

Appendix A

GenCore version 5.1.4-P5_4578
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OM protein - protein search, using sw model

Run on: March 10, 2003, 14:38:55 ; Search time 13.4774 Seconds

(without alignments)
692.052 Million cell updates/sec

Title: US-08-880-855-39
Perfect score: 1685

Sequence: 1 MRRASRDYTKYLRGSEMG.....LLDPDQDATTGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:**
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:**
- 3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:**
- 4: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:**
- 5: /cgn2_6/ptodata/1/iaa/PCPUS_COMB.pep:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1685	100.00	317	3	Sequence 137 Appl
2	1685	100.00	317	4	Sequence 137 Appl
3	1685	100.00	317	4	Sequence 137 Appl
4	1685	100.00	317	4	Sequence 137 Appl
5	1685	100.00	317	4	Sequence 137 Appl
					Sequence 13, Appl

Appendix A

RESULT 5
US-09-577-780-13 Application US/09577780
Sequence 13, Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Marskovsky, Eugene
Galbert, Laurent
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13
Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.4e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRSSEEMGGPGAPHEGPHLAPPPAPHPAPASRSMEVALLGLGLGV 60
Db 1 MRRASRDYTKYLRSSEEMGGPGAPHEGPHLAPPPAPHPAPASRSMEVALLGLGLGV 60
QY 61 VCSVALFFYFRAQMDPNRISLSEGTCHYRILRLHENDFODTTLESODTKLIPSCRIR 120
Db 61 VCSVALFFYFRAQMDPNRISLSEGTCHYRILRLHENDFODTTLESODTKLIPSCRIR 120
QY 121 QAFQAVQKELQHYVSGHRAKAMVDGSWDLAKRSKLEQPAHLITNATDIPSGS 180
Db 121 QAFQAVQKELQHYVSGHRAKAMVDGSWDLAKRSKLEQPAHLITNATDIPSGS 180
QY 181 KVISLSTWYHNRGNKAKISNMTFSNGKLIYNODGFYLYANICFRRHETSGDLATEYLQIMV 240
Db 181 KVISLSTWYHNRGNKAKISNMTFSNGKLIYNODGFYLYANICFRRHETSGDLATEYLQIMV 240
QY 241 YVTKTSIKIPSSHTLMKGSSTKYWSGSEPFHYISINVGFFKLRSGEISIEVSNPSILD 300
Db 241 YVTKTSIKIPSSHTLMKGSSTKYWSGSEPFHYISINVGFFKLRSGEISIEVSNPSILD 300
QY 301 PDQATYTGAFKVRDID 317
Db 301 PDQATYTGAFKVRDID 317

Appendix B

US-08-880-855-37.ra1

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 10, 2003, 14:38:55 ; Search time 13.4349 Seconds
(without alignments)
692.052 Million cell updates/sec

Title: US-08-880-855-37

Perfect score: 1675
Sequence: 1 MRRASRDYGYKLRSSSENGS.....LLDPDQATYFGAFKVDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCMY_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	4	US-08-989-362-2
2	1675	100.0	316	4	US-08-989-362-2

ALIGNMENTS

us-08-880-855-37.rai

QY	1	MRASADYGYKYLNSSEDMGSGPCVPEHGGPLHHPAPAPAPPPAPPAARSMEFLALGLGLG	60
QY <td>1</td> <td>MRASADYGYKYLNSSEDMGSGPCVPEHGGPLHHPAPAPAPPPAPPAARSMEFLALGLGLG</td> <td>60</td>	1	MRASADYGYKYLNSSEDMGSGPCVPEHGGPLHHPAPAPAPPPAPPAARSMEFLALGLGLG	60
Db <td>1</td> <td>MRASADYGYKYLNSSEDMGSGPCVPEHGGPLHHPAPAPAPPPAPPAARSMEFLALGLGLG</td> <td>60</td>	1	MRASADYGYKYLNSSEDMGSGPCVPEHGGPLHHPAPAPAPPPAPPAARSMEFLALGLGLG	60
QY <td>61</td> <td>VVCSIALFLFYRAQMDPNRISSEDSHFYILRLHENAIGQDSTLSEEDTLPSDCRRMK</td> <td>120</td>	61	VVCSIALFLFYRAQMDPNRISSEDSHFYILRLHENAIGQDSTLSEEDTLPSDCRRMK	120
QY <td>61</td> <td>VVCSIALFLFYRAQMDPNRISSEDSHFYILRLHENAIGQDSTLSEEDTLPSDCRRMK</td> <td>120</td>	61	VVCSIALFLFYRAQMDPNRISSEDSHFYILRLHENAIGQDSTLSEEDTLPSDCRRMK	120
Db <td>61</td> <td>VVCSIALFLFYRAQMDPNRISSEDSHFYILRLHENAIGQDSTLSEEDTLPSDCRRMK</td> <td>120</td>	61	VVCSIALFLFYRAQMDPNRISSEDSHFYILRLHENAIGQDSTLSEEDTLPSDCRRMK	120
QY <td>121</td> <td>AFQGAQVQKEIHOHTVGPQFGAPAPAMMGSLDVAQRKPEAOPFAHLITNAASIPSGSHK</td> <td>180</td>	121	AFQGAQVQKEIHOHTVGPQFGAPAPAMMGSLDVAQRKPEAOPFAHLITNAASIPSGSHK	180
QY <td>121</td> <td>AFQGAQVQKEIHOHTVGPQFGAPAPAMMGSLDVAQRKPEAOPFAHLITNAASIPSGSHK</td> <td>180</td>	121	AFQGAQVQKEIHOHTVGPQFGAPAPAMMGSLDVAQRKPEAOPFAHLITNAASIPSGSHK	180
Db <td>121</td> <td>AFQGAQVQKEIHOHTVGPQFGAPAPAMMGSLDVAQRKPEAOPFAHLITNAASIPSGSHK</td> <td>180</td>	121	AFQGAQVQKEIHOHTVGPQFGAPAPAMMGSLDVAQRKPEAOPFAHLITNAASIPSGSHK	180

QY	181	VTLSSWTHDRGMAKISMTLSNGLKLRVNODGFFYLXANICFRHETSGSVPTDYLDAMY	240
Db	181	VTLSSWTHDRGMAKISMTLSNGLKLRVNODGFFYLXANICFRHETSGSVPTDYLDAMY	240
QY	241	VVKRSIKIPSSHNLMKGGSTLRNMSGNSEPHFYSINVGFFPKLRAGEEISIQVSNPSLDP	3000
Db	241	VVKRSIKIPSSHNLMKGGSTLRNMSGNSEPHFYSINVGFFPKLRAGEEISIQVSNPSLDP	3000
QY	301	DODATYFGAFKYDID	316
Db	301	DODATYFGAFKYDID	316

Appendix B

us-08-880-855-37.ra1

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OM protein - protein search, using sw model

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File: US-08-880-855-37

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Sequence: 1 MRASRDYGYKLRSSSENGS.....LIDPDQDQTYFGAFKVDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents_AA:*
- 1: /cgn2_6/ptodata1/1aa/5A_COMB.pep:*
 - 2: /cgn2_6/ptodata1/1aa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata1/1aa/5A_COMB.pep:*
 - 4: /cgn2_6/ptodata1/1aa/5B_COMB.pep:*
 - 5: /cgn2_6/ptodata1/1aa/PCTUS_COMB.pep:*
 - 6: /cgn2_6/ptodata1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	4	US-08-989-362-2
2	1675	100.0	316	4	US-08-989-362-2

ALIGNMENTS

Appendix B

us-08-880-855-37.ra1

RESULT 2
US-08-989-362-2
; Sequence 2, Application US/08989362
; Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-362-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRARDYGYKILRSSEEMSGGPGVHEGLPHAPAPAPAPPPAASRSMFLALIGLIGQ 60
DB 1 MRRASRDYGYKILRSSEEMSGGPGVHEGLPHAPAPAPAPPPAASRSMFLALIGLIGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENGLODSTLESEDTLPDSCRMMQ 120
DB 61 VVCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENGLODSTLESEDTLPDSCRMMQ 120
QY 121 AFOGAVQKELQIHVGPOFSGAPAMMEGSLDVAQGRPEAOPFAHLTINAAISPSGSHK 180
DB 121 AFOGAVQKELQIHVGPOFSGAPAMMEGSLDVAQGRPEAOPFAHLTINAAISPSGSHK 180

QY 181 VTLSWYHDGMAKISNMTISNGKRLRVNODGFYLLANICFRHHTSGSVPTDYLQIMVY 240
DB 181 VTLSWYHDGMAKISNMTISNGKRLRVNODGFYLLANICFRHHTSGSVPTDYLQIMVY 240
QY 241 VVKTSLKIPSSHNLKMGSGTKNMGSEFHFYSINVGFFRLRAGEISIQVSNPSLIDP 300
DB 241 VVKTSLKIPSSHNLKMGSGTKNMGSEFHFYSINVGFFRLRAGEISIQVSNPSLIDP 300
QY 301 DQDATYFGAFKVDID 316
DB 301 DQDATYFGAFKVDID 316